

## SEQUENCE LISTING

&lt;110&gt; CNRS

<120> STARCH GRANULES CONTAINING A RECOMBINANT POLYPEPTIDE  
OF INTEREST, A METHOD OF OBTAINING THEM AND THEIR USES

&lt;130&gt; WOB 99 AB CNR AMYL

&lt;140&gt; US 09/980,771

&lt;141&gt; 2001-11-15

&lt;150&gt; FR 99/06494

&lt;151&gt; 1999-05-21

&lt;160&gt; 9

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 3117

&lt;212&gt; DNA

&lt;213&gt; Chlamydomonas reinhardtii

&lt;400&gt; 1

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<210> 2

<211> 2124

<212> DNA

<213> artificial sequence

<220>

<223> fragment of the complete sequence of cDNA coding  
for the GBSSI of *Chlamydomonas reinhardtii*

<220>

<221> CDS

<222> (1)..(2124)

<223>

<400> 2

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Met Ala Val Ala Ser Thr Ser Arg Pro Ser Ser Ala Arg Pro Ile Val
1 5 10 15

```

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atc aat gcc gcg tcg ttc ggt gtc aag aag acc gcg aac cag ctg ctg 96
Ile Asn Ala Ala Ser Phe Gly Val Lys Lys Thr Ala Asn Gln Leu Leu
20 25 30

```

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cgt gag ctt gct cgt ggc tcc gca cgc aag tcc acc tcg cgc tcg gct 144
Arg Glu Leu Ala Arg Gly Ser Ala Arg Lys Ser Thr Ser Arg Ser Ala
35 40 45

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gtt act ggt gcc act ggt gcc act tgc gcg ctg gac atc gtg atg gtt 192
Val Thr Gly Ala Thr Gly Ala Thr Cys Ala Leu Asp Ile Val Met Val
50 55 60

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gct gct gag gtc gcc cct tgg tcc aag acg ggc ggc ctg ggc gat gtg 240
Ala Ala Glu Val Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val
65 70 75 80

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act ggt ggc ctg cct att gag ctg gtc aag cgc ggc cac cgc gtc atg 288
Thr Gly Gly Leu Pro Ile Glu Leu Val Lys Arg Gly His Arg Val Met
85 90 95

```

```

acc att gcc cct cgc tac gac cag tac gct gac gcc tgg gac acc tcg 336
Thr Ile Ala Pro Arg Tyr Asp Gln Tyr Ala Asp Ala Trp Asp Thr Ser
100 105 110

```

gtg gtc gtg gac atc atg ggc gag aag gtc cgc tac ttc cac tcc atc Val Val Val Asp Ile Met Gly Glu Lys Val Arg Tyr Phe His Ser Ile 115 120 125	384
aag aag ggc gtg cac cgc gtg tgg att gac cac ccc tgg ttc ctg gcc Lys Lys Gly Val His Arg Val Trp Ile Asp His Pro Trp Phe Leu Ala 130 135 140	432
aag gtc tgg ggc aag acc ggc tcc aag ctg tac ggc ccc cgc tcc ggc Lys Val Trp Gly Lys Thr Gly Ser Lys Leu Tyr Gly Pro Arg Ser Gly 145 150 155 160	480
gct gac tac ctg gac aac cac aag cgc ttc gcc ctg ttc tgc aag gcc Ala Asp Tyr Leu Asp Asn His Lys Arg Phe Ala Leu Phe Cys Lys Ala 165 170 175	528
gct att gag gct gcc cgc gtg ctg ccc ttc ggc ccc ggc gag gac tgc Ala Ile Glu Ala Ala Arg Val Leu Pro Phe Gly Pro Gly Glu Asp Cys 180 185 190	576
gtc ttc gtg gcc aac gac tgg cac tcc gcc ctg gtg ccc gtc ctg ctg Val Phe Val Ala Asn Asp Trp His Ser Ala Leu Val Pro Val Leu Leu 195 200 205	624
aag gac gag tac cag ccc aag ggc cag ttc acc aag gcc aag tcg gtg Lys Asp Glu Tyr Gln Pro Lys Gly Gln Phe Thr Lys Ala Lys Ser Val 210 215 220	672
ctg gct atc cac aac atc gcc ttc cag ggc cgc atg tgg gag gag gct Leu Ala Ile His Asn Ile Ala Phe Gln Gly Arg Met Trp Glu Glu Ala 225 230 235 240	720
ttc aag gac acg aag ctg ccc cag gcc gcc ttt gac aag ctg gcc ttc Phe Lys Asp Thr Lys Leu Pro Gln Ala Ala Phe Asp Lys Leu Ala Phe 245 250 255	768
tcg gac ggc tat gcc aag gtt tac act gag gcc acc ccc atg gag gag Ser Asp Gly Tyr Ala Lys Val Tyr Thr Glu Ala Thr Pro Met Glu Glu 260 265 270	816
gac gag aag ccc ccg ctg acg gga aag acc tac aag aag atc aac tgg Asp Glu Lys Pro Pro Leu Thr Gly Lys Thr Tyr Lys Lys Ile Asn Trp 275 280 285	864
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gac acc gtc atc cgc gcc aag ggc att gag ggc att gtg aac ggc atg Asp Thr Val Ile Arg Ala Lys Gly Ile Glu Gly Ile Val Asn Gly Met 325 330 335	1008
gac att gag gag tgg aac ccc aag acc gac aag ttc ctg tct gcg ccc Asp Ile Glu Glu Trp Asn Pro Lys Thr Asp Lys Phe Leu Ser Ala Pro 340 345 350	1056

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ctg cag gcc gag ctg ggc ctg cct gtg gac ccc acc gcc ccc ctg ttc Leu Gln Ala Glu Leu Gly Leu Pro Val Asp Pro Thr Ala Pro Leu Phe 370 375 380	1152
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acc gtg ccc gtg gta gcc tcc acc ggc ggc ctg gtc gac acc gtc aag Thr Val Pro Val Val Ala Ser Thr Gly Gly Leu Val Asp Thr Val Lys 485 490 495	1488
gag ggc gtc acc ggc ttc cac atg ggc gcc ctg aac ccc gac aag ctg Glu Gly Val Thr Gly Phe His Met Gly Ala Leu Asn Pro Asp Lys Leu 500 505 510	1536
gac gag gct gac gcc gac gcc ctg gcc gcc acc gtg cgc cgt gcc agc Asp Glu Ala Asp Ala Asp Ala Leu Ala Ala Thr Val Arg Arg Ala Ser 515 520 525	1584
gag gtg ttt gcg ggc ggc cgc tac ccc gag atg gtg gcc aac tgc atc Glu Val Phe Ala Gly Gly Arg Tyr Pro Glu Met Val Ala Asn Cys Ile 530 535 540	1632
agc cag gac ctg tcc tgg tcc aag ccc gcc cag aag tgg gag ggc ctg Ser Gln Asp Leu Ser Trp Ser Lys Pro Ala Gln Lys Trp Glu Gly Leu 545 550 555 560	1680
ctg gag gag gtg gtg tac ggc aag ggc ggc gtg gcc acc gcc aag aag Leu Glu Glu Val Val Tyr Gly Lys Gly Gly Val Ala Thr Ala Lys Lys 565 570 575	1728
gag gag atc aag gtg ccc gtt gcc gag aag atc ccc ggc gac ctg ccc Glu Glu Ile Lys Val Pro Val Ala Glu Lys Ile Pro Gly Asp Leu Pro 580 585 590	1776

gcc gtg tcc tac gcc ccc aac acc ctg aag ccc gtg tcc gcc tcc gtg 1824  
Ala Val Ser Tyr Ala Pro Asn Thr Leu Lys Pro Val Ser Ala Ser Val  
595 600 605

gag ggc aac ggc gcc gcc gcg ccc aag gtc ggc acc acc gcc ccc gcc 1872  
Glu Gly Asn Gly Ala Ala Pro Lys Val Gly Thr Thr Ala Pro Ala  
610 615 620

atg ggc gcg tgg cgc gcg acc acc ccc tcg ggc ccc tcg ccc gcc gcc 1920  
Met Gly Ala Trp Arg Ala Thr Thr Pro Ser Gly Pro Ser Pro Ala Ala  
625 630 635 640

gcc acc ccc aag gtg acc acc tac aag ccc gcc ctg ccc gcc acc gcc 1968  
Ala Thr Pro Lys Val Thr Thr Tyr Lys Pro Ala Leu Pro Ala Thr Ala  
645 650 655

aag ccc aag acc gct ggc ctc aag ctg gcc ggt gag gcc tcc acc acc 2016  
Lys Pro Lys Thr Ala Gly Leu Lys Leu Ala Gly Glu Ala Ser Thr Thr  
660 665 670

tcg acc tcg gag aac ggc gct gcc tcc aac ggc aac ggc aac ggt gcc 2064  
Ser Thr Ser Glu Asn Gly Ala Ala Ser Asn Gly Asn Gly Asn Gly Ala  
675 680 685

tcg gcc tcc aag acc tcg gct gcc aag ccc ctg gtc tcc gcc gcc acc 2112  
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cgc aag tcc gcc 2124  
Arg Lys Ser Ala  
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<210> 3

<211> 708

<212> PRT

<213> artificial sequence

<220>

<223> fragment of the complete sequence of cDNA coding  
for the GBSSI of *Chlamydomonas reinhardtii*

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Arg Glu Leu Ala Arg Gly Ser Ala Arg Lys Ser Thr Ser Arg Ser Ala  
35 40 45

Val Thr Gly Ala Thr Gly Ala Thr Cys Ala Leu Asp Ile Val Met Val  
50 55 60

Ala Ala Glu Val Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val  
65 70 75 80

Thr Gly Gly Leu Pro Ile Glu Leu Val Lys Arg Gly His Arg Val Met  
85 90 95

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Lys	Lys	Gly	Val	His	Arg	Val	Trp	Ile	Asp	His	Pro	Trp	Phe	Leu	Ala	
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Lys	Val	Trp	Gly	Lys	Thr	Gly	Ser	Lys	Leu	Tyr	Gly	Pro	Arg	Ser	Gly	
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Ala	Asp	Tyr	Leu	Asp	Asn	His	Lys	Arg	Phe	Ala	Leu	Phe	Cys	Lys	Ala	
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Ala	Ile	Glu	Ala	Ala	Arg	Val	Leu	Pro	Phe	Gly	Pro	Gly	Glu	Asp	Cys	
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Val	Phe	Val	Ala	Asn	Asp	Trp	His	Ser	Ala	Leu	Val	Pro	Val	Leu	Leu	
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Lys	Asp	Glu	Tyr	Gln	Pro	Lys	Gly	Gln	Phe	Thr	Lys	Ala	Lys	Ser	Val	
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Ser	Asp	Gly	Tyr	Ala	Lys	Val	Tyr	Thr	Glu	Ala	Thr	Pro	Met	Glu	Glu	
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Asp	Glu	Lys	Pro	Pro	Leu	Thr	Gly	Lys	Thr	Tyr	Lys	Lys	Ile	Asn	Trp	
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 450 455 460  
 Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu His Ala Met His Tyr Gly  
 465 470 475 480  
 Thr Val Pro Val Val Ala Ser Thr Gly Gly Leu Val Asp Thr Val Lys  
 485 490 495  
 Glu Gly Val Thr Gly Phe His Met Gly Ala Leu Asn Pro Asp Lys Leu  
 500 505 510  
 Asp Glu Ala Asp Ala Asp Ala Leu Ala Ala Thr Val Arg Arg Ala Ser  
 515 520 525  
 Glu Val Phe Ala Gly Gly Arg Tyr Pro Glu Met Val Ala Asn Cys Ile  
 530 535 540  
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 545 550 555 560  
 Leu Glu Glu Val Val Tyr Gly Lys Gly Gly Val Ala Thr Ala Lys Lys  
 565 570 575  
 Glu Glu Ile Lys Val Pro Val Ala Glu Lys Ile Pro Gly Asp Leu Pro  
 580 585 590  
 Ala Val Ser Tyr Ala Pro Asn Thr Leu Lys Pro Val Ser Ala Ser Val  
 595 600 605  
 Glu Gly Asn Gly Ala Ala Ala Pro Lys Val Gly Thr Thr Ala Pro Ala  
 610 615 620  
 Met Gly Ala Trp Arg Ala Thr Thr Pro Ser Gly Pro Ser Pro Ala Ala  
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 Ala Thr Pro Lys Val Thr Thr Tyr Lys Pro Ala Leu Pro Ala Thr Ala  
 645 650 655  
 Lys Pro Lys Thr Ala Gly Leu Lys Leu Ala Gly Glu Ala Ser Thr Thr  
 660 665 670  
 Ser Thr Ser Glu Asn Gly Ala Ala Ser Asn Gly Asn Gly Asn Gly Ala  
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 <212> DNA  
 <213> artificial sequence

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 for the GBSSI of *Chlamydomonas reinhardtii* and  
 coding for the mature GBSSI protein

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 <222> (1)..(1953)  
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Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val	
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Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr	
35 40 45	
gct gac gcc tgg gac acc tcg gtg gtc gtg gac atc atg ggc gag aag	192
Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys	
50 55 60	
gtc cgc tac ttc cac tcc atc aag aag ggc gtg cac cgc gtg tgg att	240
Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile	
65 70 75 80	
gac cac ccc tgg ttc ctg gcc aag gtc tgg ggc aag acc ggc tcc aag	288
Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys	
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Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg	
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Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro	
115 120 125	
ttc ggc ccc ggc gag gac tgc gtc ttc gtg gcc aac gac tgg cac tcc	432
Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser	
130 135 140	
gcc ctg gtg ccc gtc ctg ctg aag gac gag tac cag ccc aag ggc cag	480
Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln	
145 150 155 160	
ttc acc aag gcc aag tcg gtg ctg gct atc cac aac atc gcc ttc cag	528
Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln	
165 170 175	



ggc cgc atg tgg gag gag gct ttc aag gac acg aag ctg ccc cag gcc Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala 180 185 190	576
gcc ttt gac aag ctg gcc ttc tcg gac ggc tat gcc aag gtt tac act Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr 195 200 205	624
gag gcc acc ccc atg gag gag gac gag aag ccc ccg ctg acg gga aag Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys 210 215 220	672
acc tac aag aag atc aac tgg ctg aag ggt ggc att atc gcc gcc gac Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp 225 230 235 240	720
aag ctg gtg act gtg tcg ccc aac tac gcg acc gag atc gct gcc gat Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp 245 250 255	768
gcc gcc ggc ggt gtg gag ctg gac acc gtc atc cgc gcc aag ggc att Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile 260 265 270	816
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gac aag ttc ctg tct gcg ccc tac gac cag aac agc gtc tac gcc ggc Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly 290 295 300	912
aag gcc gcc gcc aag gag gcc ctg cag gcc gag ctg ggc ctg cct gtg Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val 305 310 315 320	960
gac ccc acc gcc ccc ctg ttc gcc ttc atc ggc cgc ctg gag gag cag Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln 325 330 335	1008
aag ggt gtg gac atc atc ctg gcc gcc ctg ccc aag atc ctg gcc acc Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr 340 345 350	1056
ccc aag gtg cag atc gcc atc ctg ggt acc ggc aag gcc gcc tac gag Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu 355 360 365	1104
aag ctg gtg aac gcc atc ggc acc aag tac aag ggc cgc gcc aag ggc Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly 370 375 380	1152
gtg gtc aag ttc tcg gcg ccc ctg gcg cac atg ctc acc gcc ggc gcc Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala 385 390 395 400	1200
gac ttc atg ctg gtg ccc tcg cgc ttc gag ccc tgc ggc ctg atc cag Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln 405 410 415	1248

ctg cac gcc atg cac tac ggt acc gtg ccc gtg gta gcc tcc acc ggc Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly 420 425 430	1296
ggc ctg gtc gac acc gtc aag gag ggc gtc acc ggc ttc cac atg ggc Gly Leu Val Asp Thr Val Lys Glu Gly Val Thr Gly Phe His Met Gly 435 440 445	1344
gcc ctg aac ccc gac aag ctg gac gag gct gac gcc gac gcc ctg gcc Ala Leu Asn Pro Asp Lys Leu Asp Glu Ala Asp Ala Asp Ala Leu Ala 450 455 460	1392
gcc acc gtg cgc cgt gcc agc gag gtg ttt gcg ggc ggc cgc tac ccc Ala Thr Val Arg Arg Ala Ser Glu Val Phe Ala Gly Gly Arg Tyr Pro 465 470 475 480	1440
gag atg gtg gcc aac tgc atc agc cag gac ctg tcc tgg tcc aag ccc Glu Met Val Ala Asn Cys Ile Ser Gln Asp Leu Ser Trp Ser Lys Pro 485 490 495	1488
gcc cag aag tgg gag ggc ctg ctg gag gag gtg gtg tac ggc aag ggc Ala Gln Lys Trp Glu Gly Leu Leu Glu Glu Val Val Tyr Gly Lys Gly 500 505 510	1536
ggc gtg gcc acc gcc aag aag gag gag atc aag gtg ccc gtt gcc gag Gly Val Ala Thr Ala Lys Lys Glu Glu Ile Lys Val Pro Val Ala Glu 515 520 525	1584
aag atc ccc ggc gac ctg ccc gcc gtg tcc tac gcc ccc aac acc ctg Lys Ile Pro Gly Asp Leu Pro Ala Val Ser Tyr Ala Pro Asn Thr Leu 530 535 540	1632
aag ccc gtg tcc gcc tcc gtg gag ggc aac ggc gcc gcc gcg ccc aag Lys Pro Val Ser Ala Ser Val Glu Gly Asn Gly Ala Ala Ala Pro Lys 545 550 555 560	1680
gtc ggc acc acc gcc ccc gcc atg ggc gcg tgg cgc gcg acc acc ccc Val Gly Thr Thr Ala Pro Ala Met Gly Ala Trp Arg Ala Thr Thr Pro 565 570 575	1728
tcg ggc ccc tcg ccc gcc gcc gcc acc ccc aag gtg acc acc tac aag Ser Gly Pro Ser Pro Ala Ala Ala Thr Pro Lys Val Thr Thr Tyr Lys 580 585 590	1776
ccc gcc ctg ccc gcc acc gcc aag ccc aag acc gct ggc ctc aag ctg Pro Ala Leu Pro Ala Thr Ala Lys Pro Lys Thr Ala Gly Leu Lys Leu 595 600 605	1824
gcc ggt gag gcc tcc acc acc tcg acc tcg gag aac ggc gct gcc tcc Ala Gly Glu Ala Ser Thr Thr Ser Thr Ser Glu Asn Gly Ala Ala Ser 610 615 620	1872
aac ggc aac ggc aac ggt gcc tcg gcc tcc aag acc tcg gct gcc aag Asn Gly Asn Gly Asn Gly Ala Ser Ala Ser Lys Thr Ser Ala Ala Lys 625 630 635 640	1920
ccc ctg gtc tcc gcc gcc acc cgc aag tcc gcc Pro Leu Val Ser Ala Ala Thr Arg Lys Ser Ala 645 650	1953

<210> 5  
 <211> 651  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> fragment of the complete sequence of cDNA coding  
 for the GBSSI of *Chlamydomonas reinhardtii* and  
 coding for the mature GBSSI protein

<400> 5  
 Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys  
 1 5 10 15  
 Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val  
 20 25 30  
 Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr  
 35 40 45  
 Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys  
 50 55 60  
 Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile  
 65 70 75 80  
 Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys  
 85 90 95  
 Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg  
 100 105 110  
 Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro  
 115 120 125  
 Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser  
 130 135 140  
 Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln  
 145 150 155 160  
 Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln  
 165 170 175  
 Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala  
 180 185 190  
 Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr  
 195 200 205  
 Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys  
 210 215 220  
 Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp  
 225 230 235 240  
 Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp  
 245 250 255  
 Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile  
 260 265 270

Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr  
 275 280 285  
 Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly  
 290 295 300  
 Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val  
 305 310 315 320  
 Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln  
 325 330 335  
 Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr  
 340 345 350  
 Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu  
 355 360 365  
 Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly  
 370 375 380  
 Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala  
 385 390 395 400  
 Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln  
 405 410 415  
 Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly  
 420 425 430  
 Gly Leu Val Asp Thr Val Lys Glu Gly Val Thr Gly Phe His Met Gly  
 435 440 445  
 Ala Leu Asn Pro Asp Lys Leu Asp Glu Ala Asp Ala Asp Ala Leu Ala  
 450 455 460  
 Ala Thr Val Arg Arg Ala Ser Glu Val Phe Ala Gly Gly Arg Tyr Pro  
 465 470 475 480  
 Glu Met Val Ala Asn Cys Ile Ser Gln Asp Leu Ser Trp Ser Lys Pro  
 485 490 495  
 Ala Gln Lys Trp Glu Gly Leu Leu Glu Glu Val Val Tyr Gly Lys Gly  
 500 505 510  
 Gly Val Ala Thr Ala Lys Lys Glu Glu Ile Lys Val Pro Val Ala Glu  
 515 520 525  
 Lys Ile Pro Gly Asp Leu Pro Ala Val Ser Tyr Ala Pro Asn Thr Leu  
 530 535 540  
 Lys Pro Val Ser Ala Ser Val Glu Gly Asn Gly Ala Ala Ala Pro Lys  
 545 550 555 560  
 Val Gly Thr Thr Ala Pro Ala Met Gly Ala Trp Arg Ala Thr Thr Pro  
 565 570 575  
 Ser Gly Pro Ser Pro Ala Ala Ala Thr Pro Lys Val Thr Thr Tyr Lys  
 580 585 590

Pro Ala Leu Pro Ala Thr Ala Lys Pro Lys Thr Ala Gly Leu Lys Leu  
595 600 605

Ala Gly Glu Ala Ser Thr Thr Ser Thr Ser Glu Asn Gly Ala Ala Ser  
610 615 620

Asn Gly Asn Gly Asn Gly Ala Ser Ala Ser Lys Thr Ser Ala Ala Lys  
625 630 635 640

Pro Leu Val Ser Ala Ala Thr Arg Lys Ser Ala  
645 650

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<210> 6
<211> 1314
<212> DNA
<213> artificial sequence
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<220>  
<223> fragment of the complete cDNA coding for  
the GBSSI of *Chlamydomonas reinhardtii*

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<220>
<221> CDS
<222> (1) .. (1314)
<223>
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<400> 6
gcg ctg gac atc gtg atg gtt gct gct gag gtc gcc cct tgg tcc aag      48
Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys
1          5          10          15
```

acg ggc ggc ctg ggc gat gtg act ggt ggc ctg cct att gag ctg gtc 96  
Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val  
20 25 30

aag cgc ggc cac cgc gtc atg acc att gcc cct cgc tac gac cag tac 144  
Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr  
35 40 45

gct gac gcc tgg gac acc tcg gtg gtc gtg gac atc atg ggc gag aag 192  
Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys  
50 55 60

gtc cgc tac ttc cac tcc atc aag aag ggc gtg cac cgc gtg tgg att 240  
Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile  
65 70 75 80

gac cac ccc tgg ttc ctg gcc aag gtc tgg ggc aag acc ggc tcc aag 288  
Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys  
85 90 95

ctg tac ggc ccc cgc tcc ggc gct gac tac ctg gac aac cac aag cgc 336  
Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg  
100 105 110

ttc	gcc	ctg	ttc	tgc	aag	gcc	gct	att	gag	gct	gcc	cgc	gtg	ctg	ccc	384
Phe	Ala	Leu	Phe	Cys	Lys	Ala	Ala	Ile	Glu	Ala	Ala	Arg	Val	Leu	Pro	
		115					120					125				

ttc ggc ccc ggc gag gac tgc gtc ttc gtg gcc aac gac tgg cac tcc Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser 130 135 140	432
gcc ctg gtg ccc gtc ctg ctg aag gac gag tac cag ccc aag ggc cag Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln 145 150 155 160	480
ttc acc aag gcc aag tcg gtg ctg gct atc cac aac atc gcc ttc cag Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln 165 170 175	528
ggc cgc atg tgg gag gag gct ttc aag gac acg aag ctg ccc cag gcc Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala 180 185 190	576
gcc ttt gac aag ctg gcc ttc tcg gac ggc tat gcc aag gtt tac act Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr 195 200 205	624
gag gcc acc ccc atg gag gag gac gag aag ccc ccg ctg acg gga aag Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys 210 215 220	672
acc tac aag aag atc aac tgg ctg aag ggt ggc att atc gcc gcc gac Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp 225 230 235 240	720
aag ctg gtg act gtg tcg ccc aac tac gcg acc gag atc gct gcc gat Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp 245 250 255	768
gcc gcc ggc ggt gtg gag ctg gac acc gtc atc cgc gcc aag ggc att Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile 260 265 270	816
gag ggc att gtg aac ggc atg gac att gag gag tgg aac ccc aag acc Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr 275 280 285	864
gac aag ttc ctg tct gcg ccc tac gac cag aac agc gtc tac gcc ggc Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly 290 295 300	912
aag gcc gcc gcc aag gag gcc ctg cag gcc gag ctg ggc ctg cct gtg Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val 305 310 315 320	960
gac ccc acc gcc ccc ctg ttc gcc ttc atc ggc cgc ctg gag gag cag Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln 325 330 335	1008
aag ggt gtg gac atc atc ctg gcc gcc ctg ccc aag atc ctg gcc acc Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr 340 345 350	1056
ccc aag gtg cag atc gcc atc ctg ggt acc ggc aag gcc gcc tac gag Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu 355 360 365	1104

aag ctg gtg aac gcc atc ggc acc aag tac aag ggc cgc gcc aag ggc 1152  
 Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly  
 370 375 380

gtg gtc aag ttc tcg gcg ccc ctg gcg cac atg ctc acc gcc ggc gcc 1200  
 Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala  
 385 390 395 400

gac ttc atg ctg gtg ccc tcg cgc ttc gag ccc tgc ggc ctg atc cag 1248  
 Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln  
 405 410 415

ctg cac gcc atg cac tac ggt acc gtg ccc gtg gta gcc tcc acc ggc 1296  
 Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly  
 420 425 430

ggc ctg gtc gac acc gtc 1314  
 Gly Leu Val Asp Thr Val  
 435

<210> 7  
 <211> 438  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> fragment of the complete cDNA coding  
 for the GBSSI of *Chlamydomonas reinhardtii*

<400> 7  
 Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys  
 1 5 10 15  
 Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val  
 20 25 30  
 Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr  
 35 40 45  
 Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys  
 50 55 60  
 Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile  
 65 70 75 80  
 Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys  
 85 90 95  
 Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg  
 100 105 110  
 Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro  
 115 120 125  
 Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser  
 130 135 140  
 Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln  
 145 150 155 160

Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln  
                             165                            170                            175  
 Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala  
                             180                            185                            190  
 Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr  
                             195                            200                            205  
 Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys  
                             210                            215                            220  
 Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp  
 225                            230                            235                            240  
 Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp  
                             245                            250                            255  
 Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile  
                             260                            265                            270  
 Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr  
                             275                            280                            285  
 Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly  
                             290                            295                            300  
 Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val  
 305                            310                            315                            320  
 Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln  
                             325                            330                            335  
 Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr  
                             340                            345                            350  
 Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu  
                             355                            360                            365  
 Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly  
                             370                            375                            380  
 Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala  
 385                            390                            395                            400  
 Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln  
                             405                            410                            415  
 Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly  
                             420                            425                            430  
 Gly Leu Val Asp Thr Val  
                             435

<210> 8  
 <211> 1593  
 <212> DNA  
 <213> artificial sequence



<220>  
 <223> fragment of the complete cDNA coding for  
 the GBSSI of *Chlamydomonas reinhardtii*

<220>  
 <221> CDS  
 <222> (1)..(1593)  
 <223>

<400> 8  
 gcg ctg gac atc gtg atg gtt gct gct gag gtc gcc cct tgg tcc aag 48  
 Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys  
 1 5 10 15  
 acg ggc ggc ctg ggc gat gtg act ggt ggc ctg cct att gag ctg gtc 96  
 Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val  
 20 25 30  
 aag cgc ggc cac cgc gtc atg acc att gcc cct cgc tac gac cag tac 144  
 Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr  
 35 40 45  
 gct gac gcc tgg gac acc tcg gtg gtc gtg gac atc atg ggc gag aag 192  
 Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys  
 50 55 60  
 gtc cgc tac ttc cac tcc atc aag aag ggc gtg cac cgc gtg tgg att 240  
 Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile  
 65 70 75 80  
 gac cac ccc tgg ttc ctg gcc aag gtc tgg ggc aag acc ggc tcc aag 288  
 Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys  
 85 90 95  
 ctg tac ggc ccc cgc tcc ggc gct gac tac ctg gac aac cac aag cgc 336  
 Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg  
 100 105 110  
 ttc gcc ctg ttc tgc aag gcc gct att gag gct gcc cgc gtg ctg ccc 384  
 Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro  
 115 120 125  
 ttc ggc ccc ggc gag gac tgc gtc ttc gtg gcc aac gac tgg cac tcc 432  
 Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser  
 130 135 140  
 gcc ctg gtg ccc gtc ctg ctg aag gac gag tac cag ccc aag ggc cag 480  
 Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln  
 145 150 155 160  
 ttc acc aag gcc aag tcg gtg ctg gct atc cac aac atc gcc ttc cag 528  
 Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln  
 165 170 175  
 ggc cgc atg tgg gag gag gct ttc aag gac acg aag ctg ccc cag gcc 576  
 Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala  
 180 185 190  
 gcc ttt gac aag ctg gcc ttc tcg gac ggc tat gcc aag gtt tac act 624  
 Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr  
 195 200 205

gag gcc acc ccc atg gag gag gac gag aag ccc ccg ctg acg gga aag Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys 210 215 220	672
acc tac aag aag atc aac tgg ctg aag ggt ggc att atc gcc gcc gac Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp 225 230 235 240	720
aag ctg gtg act gtg tcg ccc aac tac gcg acc gag atc gct gcc gat Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp 245 250 255	768
gcc gcc ggc ggt gtg gag ctg gac acc gtc atc cgc gcc aag ggc att Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile 260 265 270	816
gag ggc att gtg aac ggc atg gac att gag gag tgg aac ccc aag acc Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr 275 280 285	864
gac aag ttc ctg tct gcg ccc tac gac cag aac agc gtc tac gcc ggc Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly 290 295 300	912
aag gcc gcc gcc aag gag gcc ctg cag gcc gag ctg ggc ctg cct gtg Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val 305 310 315 320	960
gac ccc acc gcc ccc ctg ttc gcc ttc atc ggc cgc ctg gag gag cag Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln 325 330 335	1008
aag ggt gtg gac atc atc ctg gcc gcc ctg ccc aag atc ctg gcc acc Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr 340 345 350	1056
ccc aag gtg cag atc gcc atc ctg ggt acc ggc aag gcc gcc tac gag Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu 355 360 365	1104
aag ctg gtg aac gcc atc ggc acc aag tac aag ggc cgc gcc aag ggc Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly 370 375 380	1152
gtg gtc aag ttc tcg gcg ccc ctg gcg cac atg ctc acc gcc ggc gcc Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala 385 390 395 400	1200
gac ttc atg ctg gtg ccc tcg cgc ttc gag ccc tgc ggc ctg atc cag Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln 405 410 415	1248
ctg cac gcc atg cac tac ggt acc gtg ccc gtg gta gcc tcc acc ggc Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly 420 425 430	1296
ggc ctg gtc gac acc gtc aag gag ggc gtc acc ggc ttc cac atg ggc Gly Leu Val Asp Thr Val Lys Glu Gly Val Thr Gly Phe His Met Gly 435 440 445	1344

gcc ctg aac ccc gac aag ctg gac gag gct gac gcc gac gcc ctg gcc 1392  
 Ala Leu Asn Pro Asp Lys Leu Asp Glu Ala Asp Ala Asp Ala Leu Ala  
 450 455 460

gcc acc gtg cgc cgt gcc agc gag gtg ttt gcg ggc ggc cgc tac ccc 1440  
 Ala Thr Val Arg Arg Ala Ser Glu Val Phe Ala Gly Gly Arg Tyr Pro  
 465 470 475 480

gag atg gtg gcc aac tgc atc agc cag gac ctg tcc tgg tcc aag ccc 1488  
 Glu Met Val Ala Asn Cys Ile Ser Gln Asp Leu Ser Trp Ser Lys Pro  
 485 490 495

gcc cag aag tgg gag ggc ctg ctg gag gag gtg gtg tac ggc aag ggc 1536  
 Ala Gln Lys Trp Glu Gly Leu Leu Glu Glu Val Val Tyr Gly Lys Gly  
 500 505 510

ggc gtg gcc acc gcc aag aag gag gag atc aag gtg ccc gtt gcc gag 1584  
 Gly Val Ala Thr Ala Lys Lys Glu Glu Ile Lys Val Pro Val Ala Glu  
 515 520 525

aag atc ccc 1593  
 Lys Ile Pro  
 530

<210> 9  
 <211> 531  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> fragment of the complete cDNA coding for  
 the GBSSI of *Chlamydomonas reinhardtii*

<400> 9  
 Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys  
 1 5 10 15

Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val  
 20 25 30

Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr  
 35 40 45

Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys  
 50 55 60

Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile  
 65 70 75 80

Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys  
 85 90 95

Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg  
 100 105 110

Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro  
 115 120 125

Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser  
 130 135 140

Ala	Leu	Val	Pro	Val	Leu	Leu	Lys	Asp	Glu	Tyr	Gln	Pro	Lys	Gly	Gln	
145					150					155					160	
Phe	Thr	Lys	Ala	Lys	Ser	Val	Leu	Ala	Ile	His	Asn	Ile	Ala	Phe	Gln	
				165					170					175		
Gly	Arg	Met	Trp	Glu	Glu	Ala	Phe	Lys	Asp	Thr	Lys	Leu	Pro	Gln	Ala	
			180					185					190			
Ala	Phe	Asp	Lys	Leu	Ala	Phe	Ser	Asp	Gly	Tyr	Ala	Lys	Val	Tyr	Thr	
		195					200					205				
Glu	Ala	Thr	Pro	Met	Glu	Glu	Asp	Glu	Lys	Pro	Pro	Leu	Thr	Gly	Lys	
	210					215					220					
Thr	Tyr	Lys	Lys	Ile	Asn	Trp	Leu	Lys	Gly	Gly	Ile	Ile	Ala	Ala	Asp	
225					230					235					240	
Lys	Leu	Val	Thr	Val	Ser	Pro	Asn	Tyr	Ala	Thr	Glu	Ile	Ala	Ala	Asp	
				245					250						255	
Ala	Ala	Gly	Gly	Val	Glu	Leu	Asp	Thr	Val	Ile	Arg	Ala	Lys	Gly	Ile	
			260					265					270			
Glu	Gly	Ile	Val	Asn	Gly	Met	Asp	Ile	Glu	Glu	Trp	Asn	Pro	Lys	Thr	
	275						280					285				
Asp	Lys	Phe	Leu	Ser	Ala	Pro	Tyr	Asp	Gln	Asn	Ser	Val	Tyr	Ala	Gly	
	290					295					300					
Lys	Ala	Ala	Ala	Lys	Glu	Ala	Leu	Gln	Ala	Glu	Leu	Gly	Leu	Pro	Val	
305					310					315					320	
Asp	Pro	Thr	Ala	Pro	Leu	Phe	Ala	Phe	Ile	Gly	Arg	Leu	Glu	Glu	Gln	
				325					330					335		
Lys	Gly	Val	Asp	Ile	Ile	Leu	Ala	Ala	Leu	Pro	Lys	Ile	Leu	Ala	Thr	
			340					345					350			
Pro	Lys	Val	Gln	Ile	Ala	Ile	Leu	Gly	Thr	Gly	Lys	Ala	Ala	Tyr	Glu	
		355					360					365				
Lys	Leu	Val	Asn	Ala	Ile	Gly	Thr	Lys	Tyr	Lys	Gly	Arg	Ala	Lys	Gly	
	370					375					380					
Val	Val	Lys	Phe	Ser	Ala	Pro	Leu	Ala	His	Met	Leu	Thr	Ala	Gly	Ala	
385					390					395					400	
Asp	Phe	Met	Leu	Val	Pro	Ser	Arg	Phe	Glu	Pro	Cys	Gly	Leu	Ile	Gln	
				405					410					415		
Leu	His	Ala	Met	His	Tyr	Gly	Thr	Val	Pro	Val	Val	Ala	Ser	Thr	Gly	
			420					425					430			
Gly	Leu	Val	Asp	Thr	Val	Lys	Glu	Gly	Val	Thr	Gly	Phe	His	Met	Gly	
		435					440					445				
Ala	Leu	Asn	Pro	Asp	Lys	Leu	Asp	Glu	Ala	Asp	Ala	Asp	Ala	Leu	Ala	
	450					455					460					

Ala Thr Val Arg Arg Ala Ser Glu Val Phe Ala Gly Gly Arg Tyr Pro  
465 470 475 480

Glu Met Val Ala Asn Cys Ile Ser Gln Asp Leu Ser Trp Ser Lys Pro  
485 490 495

Ala Gln Lys Trp Glu Gly Leu Leu Glu Glu Val Val Tyr Gly Lys Gly  
500 505 510

Gly Val Ala Thr Ala Lys Lys Glu Glu Ile Lys Val Pro Val Ala Glu  
515 520 525

Lys Ile Pro  
530